

## FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTGGGACTTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCCTTC  
CTTACACTTCGCCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA  
CTGCTTTTTTTCCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAAACTTACT  
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT  
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAAACGGATCCTGTACAAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG  
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG  
ATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTCACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTAATCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAAGGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTAAAGGTTACATGGAAGGTTATAGCTTTG  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKL GDP  
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNLGYFFSIYCVWKIFMATINIVFDRVGKTD PVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY  
FVSSVLLIRMSMPLEYRTIITEVLGELQNFYHRWFDVIFLVSALSSILFLYL AHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## FIGURE 5

AGCAGGGAAATCCGGATGTCCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
 GTTTCCTGGCTCTGAAGGGGTAGGCACATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
 GTCATGCAGAATTATGGGGATCACCCCTTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG  
 AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGCCCGGCAAGGACCAAGTTGAAACAGCC  
 TTGAAAGCTAGCTTTGAAACTTGAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAG  
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGAAGGTTCCAGTGA  
 GCCGACAGTTTGAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
 ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGCAACACAAACAGAAATTTATTGT  
 CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC  
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG  
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTGAAAATAAAGCAGCATTCAAGAATGA  
 AGCTGCTGGGTGGAGGTGTCCTACGGCTCTGCTAGTGCTTGTCTCTCTCTTTGGTGTCTG  
 CAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT  
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAA  
 TGAGGAATCAAAGAAAACCTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC  
 GATGCTTGAAGCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCCTTT  
 CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCT  
 TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGAC  
 CTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTG  
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCCTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAAAT  
 GGCAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA  
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC  
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTGAACACACACA  
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
 AAAATAAAACCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
 ACTCAGTAATTTGTTTAAAAGTAATAAAATTCACAAACATTGCTGAATAGCTACTATATGTC  
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAATTGCACATAGTAG  
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTCTAGCTTATCTACTTCCAAACTAAT  
 TTTTATTTTGTCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT  
 TATTATTAACATACCTAAGAAGTACATTGTACCTCTATATACCAAGCACATTTTAAAAGTGCC  
 ATTAACAAATGTATCACTAGCCCTCCTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLLSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIENTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
RKKLICVTEVFEMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNNEESKKTDKNPESKSPSKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCCGGC  
GGCCTCCCGGCGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCG  
GCTCTCAGCTACCCGCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTAT  
GGAGGACACGCAGCACAAATGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC  
TGGAACAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGSGAGCTAGAGCCTGATGGAGCCTTGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG  
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGTGACCAGGCTTCTTCCTA  
CATCTTCTTCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTTCAGCT  
CCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGTCTGGGAGAGTCAGGCAGGGTTAAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG  
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG  
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCAGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCLTRDSECCGDQLCVWGHC  
TKMATRGSNGTICDNQRDCQPGGCCAFQGRLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAAALLGEEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144



## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTCTGGACCCTT  
AACTGGGTACTGGCCCTGGGCAATGCGTCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTTGGAGCCCTCATCTGACCCTTGTGCAGATAGCCCGGGTCACTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTGCCTCGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAAA  
AAGATTTTATTAAAGATATTTTGTTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGGLFWTL  
NWVLALGQCVLAFASFYWAFHKPQDIPFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPDNKKRKK

### **Important features:**

#### **Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### **N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

#### **Hypothetical YBR002c family proteins.**

amino acids 276-288

#### **Ammonium transporters proteins.**

amino acids 204-231

#### **N-myristoylation sites.**

amino acids 60-66, 78-84

#### **Amidation site.**

amino acids 306-310

## FIGURE 11

GCCCCGCGCCCGGCGCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCCTGGGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCGGGCGTGAGAGTCACTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC  
GGGATCCCCACCGTCTGACGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGTGTCTACCG  
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTTTTCACCTGCTCATGCTCTGCGTGAGCAGCA  
GCGGGGACCCCGGCTGCCATCCAGAATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC  
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCAACATCTGGTCTACTTCGGCGTGTGGG  
CTCCTTCTCTTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTCGCGACTCCTGGAACAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTC  
TTCTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTAATACTGAGCCAGCGGTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCATTTGCCAACCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCGGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG  
TGGGCCTCATCATCTTCTCTCTGTGCACCTCTTTCATCAGTCTGCGTCTCCTCAGACCACCGGCAGGT  
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTACCTACAGTACTCCTTCTTCC  
ACTTCTGCCTGGTGTGGCTCACTGCACGTGATGATGACGCTACCAACTGGTACAAGCCCGGTGAG  
ACCCGGAAGATGATCAGCAGCTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT  
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTAGGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC  
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGC  
CTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCTCTTCTTCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA  
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACCACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCAGGGGACCTGCCCCCTTCTCTG  
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCSCGAPCILCSCCPASRNSTVSRLIFTFFFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
GGTTGGAAGAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTTCTGCGCAGTTTTTCGATTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG  
TGATCCTTTTCAAGCTTTTCTCTCAAGGGGCTTTTGCTATGTGCTGCCCATCATTTTCATTTCATC  
CTTGCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTTATTTCATTCAC  
AGAATGGAATTTTTTGTTCATGTCTCAGATTTATTTGTATTTCTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTTTCTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLPOEAEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

#### **N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCGGGCCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCCCTGCCCCCGCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAGATGTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT  
 CCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGGCCCTGCCGGCTGCAGCTCCTGGACCTGTACAGAACCCAGATCGCCAGCC  
 TGCCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCCCAACCTCCACGACC  
 TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACG  
 CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGGTTTGGCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCA  
 CTTCGCCCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG  
 CCACCACCACACAGCCACAGTGGCCACCACGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTC  
 CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACG  
 GGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGCCCCAGCCCTACACCAGTACAGCCGAG  
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCAACCA  
 GCTGCGGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGGGTGCCGGAGG  
 GCGAGGAGGCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCAGTCACC  
 CAGGCCCCGCGAGGGCAACCTGCGGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGCTGCGGTGGGGGCGAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAGGGGAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAGGGAGTGAAGTCCCCTTGGAG  
 CCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCAGGGCCTGGCCCTCCAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCCTCTGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGTTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGCGCGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAACTGGAAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT  
 GGGAAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA  
 GGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDANVE  
ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNSLSQALPGDLSGLFPRLRLLLAAARNPFNCVCLSWFGPWWRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGFVPQPDCCPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTSPPTP  
VTPRPPRSLTGLIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCVMPLGPRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAGVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGLQSPHLAKPYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 579-599

#### **EGF-like domain cysteine pattern signature.**

amino acids 430-442

#### **Leucine zipper pattern.**

amino acids 197-219, 269-291

#### **N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

#### **Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

#### **N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646



## FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTAGAAGAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAGTGTACAG  
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA  
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT  
TTTCTTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG  
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAAATCCTTAATGGAAG  
CAATAAGAAAAGCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGCTCTTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCCAAAGGCTCTTGTATATTATACAT  
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTTGGTAAGTAGACTTTAGTGGAAGGCT  
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTCAGCTTTCATGATC  
CAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTCCTTCAAATCTTGTTAATGGATAT  
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAATGATTAG  
TTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG  
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA  
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTTGCAACAATGC  
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAAATGACTCCAGAGAGCTCTACTTTCTG  
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG  
AAGATTAACTCATTTTAAATAAAATTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 18**

MRVRIGLTLILLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPFLFLDK  
EYDECTSDGREDGRLWCATTYDYKADEKKGFCETEEEAARRQMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYL PQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGCNLI AHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCCATTTCTGCAGTGAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG  
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT  
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT  
CCCGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
TATGCAGTGAAGGTTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA  
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACCTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLEFWVLGILLICGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKVQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCLIEPGLFKTNLADFPVKVIEKKLAIWEQLSPDIKQQYGEYIEKSLDKLGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
CATTAGAAATATATTCCATGCTATCAGCTTTTCTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGCAGGAGCATT  
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCTTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGTT  
GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTCCTGTATGTCCACTGG  
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTTTCTTTGTGAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTT  
ATGTCTTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT  
GAGCAGCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC  
TGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA  
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
GAGACCATGTCTATTAAAAATAAAATGGAAGCAAGAATAGCCTTATTTCAAATATGGAAG  
GAAATTTATATGAAATTTATCTGAGTCATTAAAAATTCTCCTTAAGTGATACTTTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEGEVKGAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLHSYKPKQGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDDVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDLDQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 75-79, 322-326

#### **N-myristoylation site.**

amino acids 184-154

#### **Growth factor and cytokines receptors family.**

amino acids 134-150

年份	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																							
总人口	115964	116722	117480	118238	119000	119760	120520	121280	122040	122800	123560	124320	125080	125840	126600	127360	128120	128880	129640	130400	131160	131920	132680	133440	134200	134960	135720	136480	137240	138000	138760	139520	140280	141040	141800	142560	143320	144080	144840	145600	146360	147120	147880	148640	149400	150160	150920	151680	152440	153200	153960	154720	155480	156240	157000	157760	158520	159280	160040	160800	161560	162320	163080	163840	164600	165360	166120	166880	167640	168400	169160	169920	170680	171440	172200	172960	173720	174480	175240	176000	176760	177520	178280	179040	179800	180560	181320	182080	182840	183600	184360	185120	185880	186640	187400	188160	188920	189680	190440	191200	191960	192720	193480	194240	195000	195760	196520	197280	198040	198800	199560	200320	201080	201840	202600	203360	204120	204880	205640	206400	207160	207920	208680	209440	210200	210960	211720	212480	213240	214000	214760	215520	216280	217040	217800	218560	219320	220080	220840	221600	222360	223120	223880	224640	225400	226160	226920	227680	228440	229200	229960	230720	231480	232240	233000	233760	234520	235280	236040	236800	237560	238320	239080	239840	240600	241360	242120	242880	243640	244400	245160	245920	246680	247440	248200	248960	249720	250480	251240	252000	252760	253520	254280	255040	255800	256560	257320	258080	258840	259600	260360	261120	261880	262640	263400	264160	264920	265680	266440	267200	267960	268720	269480	270240	271000	271760	272520	273280	274040	274800	275560	276320	277080	277840	278600	279360	280120	280880	281640	282400	283160	283920	284680	285440	286200	286960	287720	288480	289240	290000	290760	291520	292280	293040	293800	294560	295320	296080	296840	297600	298360	299120	299880	300640	301400	3021

[illegible]

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH  
LYMQNSELFKDLFVELKRYVVGNVNLEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRL  
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFQGC GPPKPLPAGRISRISSESASFARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSLP SNVCN DERMAAGNGNEDDCWNGKGKSRYLFAVTGNLANQGNNPEVQVDT  
KPDILILRQIMALRVMTSKMKNA YNGNDVDFDISDESSGEGSGGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

#### **N-glycosylation site.**

amino acids 514-518

#### **Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

#### **N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

#### **Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506



## FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG  
AGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGCTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC  
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAGCTACTTCCCCTACCTGA  
TGGCCGTGCTGACTCCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC  
CACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA  
AGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG  
CTCTGTGCAGAGCCCAAGGAAGTCTGCAGGAGTCCGGAGAGTACTGAGACCGGAGGTGTGC  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTC  
GAGCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
GAACGCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA  
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTC  
CCAATGTTGTCCCTTTCTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACAC  
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAEMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLFPVGPHIMGKAVKQSFPPSSKALICSFPSL  
QLEQATHQPIYPLRG

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG  
CCTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

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## FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATCTAAGTGGAATCATGTCGG  
 GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC  
 TTCAGATTCAACACCCCTTCTGGTTCACATTTTCATTTATTGGTTATTTTGGGATTGTTGTT  
 TGCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
 CAGAAAGGGAAAAATATGAAGTGCCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
 CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
 AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT  
 ATGGAAGGCGGCCAAGTGAATATAAGCCCTTTTCGGGCATTGGTACATGTGGTCTGACCATTT  
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGGCTGCCAGCAAATGACTATAGCTGGGGCAG  
 TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC  
 TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG  
 GATTCCGAGAATCATTTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
 AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
 ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
 TTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
 AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
 CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC  
 TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
 AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA  
 GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT  
 TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTT  
 TAAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE  
LDTERENMKCVLGFIAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGT VVKGSFLISVVRIPRIIVMYMQNALKEQQHG  
ALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348



## FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTTAGA  
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCAATCTGTGTGGT  
 GAAAATTTTTTGAAGAAAAAATGTCCTTCTTCAAACAAGGGTGTCATTCTGATATTTATGAGGAC  
 TGTGTCTCTACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGGCTGGTGAAGTAC  
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAAGGCCCAAGTTCAGTGTGCCTCAGATCAACTGC  
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA  
 CCCCATAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG  
 TACACAGTGGTGTGCTTGATAATTGAGGAGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT  
 GGTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT  
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGAACCTACCCATCAGCTCTTACATACTCATCAT  
 CGAAAAGTCCAGCTGCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG  
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
 CACCTTGCCCAAGGCATCCCCCTTCTGCTGCTTCTACCACCAGCATCCCAGACCACAATCGATGG  
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC  
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC  
 GGATGTCAGCCTGGGACTTGTTCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
 TGGGAGATCCAACTGCAAAATGACTTGTCTGTTTTTAATTGATGGGAGCACCAGCATGGCAAA  
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGC  
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC  
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAAT  
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAAGTCTTTTTTCAAAGCCAATGGAACAGAAGCGG  
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 GACTTGGGAGAGAGTCAGGAATCAACATTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG  
 AAGCAGTATGTGGTGGAGCCCACTTTGCAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC  
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCTGCAGCCTCTGGTGAAGCGGGTCTGCG  
 ACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTCGCTGACATTGGCTTCGTCATCGAC  
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCAA  
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC  
 TGGAGTTTGGGTTGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC  
 TACTGGAGTGGTGGCACCAGCAGCGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
 GTCCAAGCCCCAAGAGGAAGTTAATGATCCTCATCACCAGCGGAGGTCTACGACGACGTCC  
 GGATCCCAGCCATGGCTGCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCTGGGCT  
 GCCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCCGCCAGAGACCACTCCTTCTTTGTGGACGA  
 GTTTGACAACCTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC  
 AGCCTCGGAACTGAATTTCAGAGCAGGCAGAGCACCAGCAAGTGTCTTTACTAAGTACGTGTT  
 GGACCAACCCACCGCTTAATGGGGCAGCAGCGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC  
 AAATGTCTTGTTATTATTCTTTGCCATCATGCTTTTTCATATTCCAAAACCTGGAGTTACAAAGA  
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT  
 TTTGACAATTGTTTTCAAAATAAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG  
 AGCTTTTGTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCAT  
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAAATGTTTAGAAGGATGAAAAATAAAAAA  
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## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR  
ESFIVLESKPKKGVTPYSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQFVTLMQLLAVTVAVA  
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPGAAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLLQPLVKRVCDDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLFEGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL  
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFF  
VDEFNLHQYVPRIIQNICTEFNSQPRN

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 181-200

#### **N-glycosylation sites.**

amino acids 390-394, 520-524

#### **N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### **Amidation site.**

amino acids 304-308

## FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTA  
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGAATGGCCTCGGCTCTCTGAGCTGTCCCTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTTCTGGTCATTTC  
TGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC  
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA  
ACCTGACCTTGAAACCATTTATGGCATTCAAGTGGGTAAGTGAAGTTTGCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA  
GAAGTTTTTTCACAGGTTATCCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAAACCCATATTT  
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAATGTCCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGGTACGTTAAACCCATCAAGTTTGAAGATGTTTATGTCGGGAT  
CTGTTTGAATTTATTAAAGTGAACATTCATATTCCAGAAGACACAAATCTTTTCTTCTATATAGAATCC  
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT  
TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTTGTGGAAGTGTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTT  
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
ACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA  
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATA  
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTACAGTTATT  
ATTATTTAAATTAATTTCACTTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG  
TGAATCATTTCTTACATGCAAACATTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA  
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT  
AATATAGAGAAGAATTAAGCAAGAAAATCTGAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNKYVMKTDVDFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 20-39

#### **N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

#### **Glycosaminoglycan attachment site.**

amino acids 239-243

#### **Ly-6 / u-PAR domain proteins.**

amino acids 23-37

#### **N-myristoylation site.**

amino acids 271-277

## FIGURE 37

CGCTCGGGCACCAGCCGCGCAAGGATGGAGCTGGGTTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC  
TCGTCTTGGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTGTCGGGAGTGCTGTG  
AATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGTGAAGAGCTGCCGAAATGGCTCATGGGGGGGT  
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTTCATGC  
TAAACCTGGGTTTGTATCCAACTAAGATTTGTATGTTGAGTCTGGAGTTTGGACTACATGTGCCAGTATGACTATGTTGAG  
GTTTCGTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCCCTGTTTCCATGACGGCACGTGCGTCCCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTTGGGGGCCAGTCAATGGGTACAGAAAA  
TAACAGGGGGGCTTGGGCTTATCAACGGGACGCCATGCTAAAATTTGGCACCGTGGTGTCTTTCTTTTGTAACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGCAGCAGAAATGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAAGCTGCCGA  
GAACCAAAGATTTAGACCTGGTGAAGAGGAGATTTCTCCGATGCAGGTTCACTCAAGGGAGACACCATTACACAGCTAT  
ACTCAGCGGCCCTTACGCAAGCAGAACTGCAGAGTCCCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAATTTGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCGAGGAGCCATCTACAGGAGGACCAGCGGGGTGCTGACGGCAGCCTACCAAGGGAGC  
GTGGTTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTTCTGCTATCATCTGCAATCCCAACTATGACCCCATCTGCTTGTGCTGACATCGCCATCTGAAAGCT  
CCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCGAGTCGGGATCTCAGCACTTCTTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG  
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATGCAAGACAGGAGGCATCGCGCTGTGCTCTCCCGGGA  
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACCTCCTGAGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCCGTAAGTGTGATTTGGCCTGTGAACCTTGGCT  
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAATTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG  
GCCCCCTTTTGGGCTCTCAAGTTCTAGAGAGCTGCCCTGTGGGACAGCCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTAATAAAATAAGGGTTGGCTTCT  
GAAC TACAAA  
AAA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRVCGNERPAPIQSIGSSSLHVLFSHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCMNSYVLSGNE  
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLSAPTK  
KPALEPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWFPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFQESHITVAGWNVLADVRSPGFKNDFLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFKVLFPKDWI  
ERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAAGGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATTTCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC  
TGGTCTTGCCTTGGCTCAGTCTGTAACTACATTGACAATGTGGGCAACCTGCACCTTCTGTATTGAGAACTCTGTA  
AAGGTGCCTCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCTTGGCTAGACA  
ACCCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA  
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA  
GGACAAAAGACGGGAGTGCAATTGCCAACCATGCCGACCGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCA  
GCAGGAACAATGGACAGGCCCGGATGCCACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGGATAAAATGCTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCCAGAAAGTGCGGCTCATCTGATTAGGCCAGTGAAGACGTGTTACCTCGTGTGTCGCCAGGTTTCGGCAGC  
GGAGCCCTGACATCTTTGAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGTGAATCTCTCG  
GCATGACCGTCGCAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACAGAGAGTCAAGC  
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCATCCT  
GGGTCAATGTGGCTGGAATTACCACGGTGTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGAATCAATGATGGGTGAGGAAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC  
TTGTGAGTTTTTATATTTAAAGAAAGAAATACATTGTAAAAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCAAAAAAATTAAGAACTACTAGTTTTTTTTTTCAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTTTATATTTTTCTATTCAATAAAAAGCCCTAAACAATAAATGATTGATTGTATATCCCACTGAATT  
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT  
AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAAGAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPESELSIRLV  
GGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDS FHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQ RSPDIFQEAGWNSNGSWSPG  
PGRSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHREWDLP IYVISVEPGGVISRDGR  
IKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPF  
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPF FIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

#### **Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

#### **N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609



## FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTTCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC  
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCC  
ATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
GACAACGTCTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
CTTTACAGAGGGTGCCTCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG  
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTTATATCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACCAACTACTGGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG  
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC  
TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCT  
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTGAAGTAATATATATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATACAATACTGTTATTCAATTATCCTGTACAATCATCTGTGAAGTGGTGGTGCAGGT  
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTTCTATTAGT  
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
ATTAATAATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

## **FIGURE 42**

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIVYVHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTTALSREQFFKVNGFSNNYWGWWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

#### **Xylose isomerase proteins.**

amino acids 191-202

## FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG  
ACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCCTCCC  
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLILLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCHRSKCGMCCKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-24

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

#### **N-myristoylation site.**

amino acids 44-50

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG  
AAACTCCTAACATATGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGAT  
GGAAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCCTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLITCCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 224-250

#### **Leucine zipper pattern.**

amino acids 229-251

#### **N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTTCATTGAAAACATCAGTGACATTCATCCAGAATCCTTCAA  
CTTGCACTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTTtaggtctattgcttgttggaattctggaggtcctgtttgggct  
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLVLLVLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKKRACNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12



## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCCAAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
**CATGG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCT**TGAG**CACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGCAGGCTGTTAGGCCCTT  
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPILITPGSATTC

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domain:**

amino acids 36-59

#### **N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

amino acids 1-16  
amino acids 36-59  
amino acids 41-47, 45-51, 84-90  
amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCCCTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
GTGCTTGGCCACAGTGGTGTCTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCCG  
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTGAGG  
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG  
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAACAAGGACCAGAGAAGCTCTC  
GCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCTCCTTAA  
AACACCACCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
AA  
AA

## FIGURE 52

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPFGGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWQGVF  
GHSGAWETSGGHGIFGSQGGGLGGQCGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF  
GTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS  
SSGSSSGSSSGSSGGSSGGSSGNSGGSRGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNE  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLLGGSGDNRYRGQSSWGSGGGDAVGGVNTVNSETPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

### Signal peptide:

amino acids 1-21

### N-glycosylation site.

amino acids 265-269

### Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

### Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

### N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

### Cell attachment sequence.

amino acids 301-304

## FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCC  
CACAGCCCCCAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCATTTC AACATCCT  
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGGAGCAGTCGCTGACATGTTTGGACATCAGCCTCATGACCTTGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGAGACTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCCGTGTCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGGCGTCCGACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTCCGCA  
GGGCCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT  
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCACTGACTTTCTGAC  
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFFQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGILLSGGDKWSRHRMLTPAFHFNIKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFDVAVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDEGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHNPTVWPDPEVYDPFRFDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

### **Important features:**

#### **Transmembrane domains:**

amino acids 13-32 (type II), 77-102

#### **Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

#### **N-glycosylation sites.**

amino acids 112-116, 168-172

## FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCACTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTTGCCGTGTGTCTTGC  
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACCTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGACGAATGTGTGCTT  
GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATCCCATGAATACAAACCTATTCAGCAACAGCAAAAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72



## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCAGCCAGCAGGCCGCCAATGCTCTGTCTGTGCCTG  
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTCCTCACCTACCGCCAGTGGAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCCGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAATTCCTCAAGAGCATGGATAAAACGGCAGCATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACCTCCTCCACCCCGTGGAAAAACATCCCGAGATCATCCTCTACTGGAAGCATCCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA  
CACCTTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGTCTATG  
CAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGG  
TCACCTTGGCGGGCAATGGCATCAACGTCTCAAAATTGCCCGGAATCAGCCATCAAATTCATGGCCTATGAGCAG  
ATCAAGCGCCTTGTGGTAGTGACCGAGAGCTCTGAGGATTACGAGAGGCTTGTGGCAGGGTCCCTTGGCAGGGGCC  
ATCGCCAGAGCAGCATCTACCAATGGAGGTCCTGAAGACCCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA  
ATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTG  
GGCATCATCCCTATGCCGGCATCGACCTTGCACTACGAGACGCTCAAGAATGCCTGGCTGCAGCATTATGCAGTG  
AACAGCGCGGACCCCGGCTGTGTGTCTCTGGCCTGTGGCACCATTGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCCGGCCCTAGTCAGGACCCGATGCAGCGCCCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAACATATCTGCGGACCCAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCCACTTCATGAAGTTCATCCCA  
GCTGTGAGCATCAGCTACGTGGTCTACGAGAACCTGAAGATCACCTTGGCGCTGCAGTGCAGCTGGAGGGGAGGGC  
CGCCCGGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT  
AAGCTGTCTCGAGCCAGCTGTGAAAACCTTAGACGCACCCGAGGAGGGTGGGGAGAGCTGECAGGCCAGGGCTT  
GTCCTGCTGACCCAGCAGACCCCTCTGTGGTTCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAGCAGG  
CTCCGGGCTCACATGTGTAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT  
TAGTTCTTCCATTTACCCCTTGACGCGAGCTGTGGCCACGGCCCTGCCCTCTGGTCTGCGCTGCATCTCCCTGTGC  
CCTCTTGTCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGCTACAGCCACATCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCCTGACTTCCCAACCTACAGCATGACGCCAATTTGGC  
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTSCAGGGGGCTCGGGCTGCCCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTTGAGGGCGAAGGGCAGAGCGTTTGTGTGTCTGGGGAGGGAAGGAAAGGTGTGGAGGCCCTTAATTATGG  
ACTGTTGGGAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTCCAGAGGAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTCTCTGTCCAACCCAGCAGGGGCCGAGC  
GGGACAGCCCCACATTTCACTTGTGTCACTGCTTGGAACTATTTATTTGTATTTATTTGAACAGAGTTATGTCTT  
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCAATTTTCAAGTTCAATTTTATTTCATATTTATGTTTCATGGTT  
GATTGTACCTTCCCAAGCCCCCAGTGGGATGGGAGGAGGAGGAGAGAGGGGGGCTTGGGCCGCTGCAGTCACATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAACGCGCCAGAAGGCAGCAGCCCTGGCTCCTTTCTTTTGGCAG  
GTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGCGTGGAGAGAGGGGAGGAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG  
TGAGGTGCCCTCTCACTGTGAATTTGTGGTGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGCTCCCTCCAGC  
CTTCTGCTGCCCTTGCTTAACAATGCCGGCCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAATGACCTGA  
TGAGGAAATCTCAATAGGATGCAAGATCAATGCAAAAATTGTTATATATGAACATATAACTGGAGTCTGTCAAAAAG  
CAAATTAAGAAAGAAATTGGAGCTTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAGTTGTTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSI FKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG  
QLDFEEFVHYLQDHEKKLRLVFKILDKNKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMKNG  
TMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRHVLVAGGG  
AGAVSRTCTAPLDRKVLQMVASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK  
FMAYEQIKRLVGSQDETLEIRHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation sites.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTTTGGTATTTTCAAGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAAACCTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTCCGAGCAGGATGAAATGTTTCAAGGCCGACAGCAGTGTGCTGATCAAGTGATAGTT  
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC  
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC  
CAGCTTTGAGCTGAACCTCTGAGAATGTGACCATGAAGTTGTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT  
GTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
TCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYMLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 258-281

#### **N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

#### **N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT  
GGGCTTTATGGACAGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGGCCCTGGTCAACTGCA  
ATTGGTCTTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTCTTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG  
AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCAAAGTGGAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCATAAAT  
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTGCAATTTTTTTC  
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQCPCGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSH  
SGYISMKELKQALVNCNWSSFNDETCIMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

## FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA  
AGCGCTGCCTGAAGAATCTCTTACCTTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCGCTGATCACCCCTGGGGTACCCTGAATCCCACTG  
TGTCTGGGGAGGTGGAGGCCCTGGGACTGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGTGGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCTATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC  
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGSPNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRNSNLGAGGKILSQRP  
PWSLIHRVLPDHPWGTNLNPSVSWGGGGPGTGWGTRMPHPEGIWGINNQPPGTSGWNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310



## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCACCCCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGLPLVLLLTLLGSSHGTPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGC  
CAGGTGCCCCGTCGCAGGTGCCCCTGCCGGAGATGCGGTAGGAGGGCGAGCGGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTTGTGCCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLLRWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 56-80

#### **N-glycosylation site.**

amino acids 36-40

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

#### **Tyrosine kinase phosphorylation site.**

amino acids 86-94

#### **N-myristoylation sites.**

amino acids 7-13, 26-32

## FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTGTCTTCTAGTTCGTGCTGCTGCACCAG  
 TCAAATACTTCTTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCTTGTATAGATCCTAGTGTGCCAGAA  
 GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
 TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAACATGAA  
 AACATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACCAAGCAGTTCACA  
 GAATGTGGAGAGAAAGCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
 CCAGGCCAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC  
 TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGCTAGAAATAGAGTTTATAAGTGT  
 CAAGGAGGCGAGTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAATGTATGGAAAAGATTGTCAATTCTTT  
 CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA  
 AAAACCCATAATCAAGAAGCTCCAAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT  
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA  
 AGAATTTGTGTCTTAGTCTTGTATAAGTCTGGAAGCATGGGGGTAAGGACCGCCTAAATCGAATGAATCAAGCAGCA  
 AAACATTTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACCTTGTATAGTACTGCCACTATTGTA  
 AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA  
 ACTTCCATCTGCTCTGGAATTAATATGCATTTCAAGTGATTGGAGAGCTACATTTCCAACTCGATGGATCCGAAGTA  
 CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGTATTGATGAAGTGAACAAAGTGGGGCCATTGTTTCT  
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
 TCAGATGAAGCTCAGAACATGGCCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAG  
 TCCCTTCAGCTCGAAAGTAAGGGATTAACTGATAGTAATGCCTGGATGAACGACACTGTCAATAATTGATAGTACA  
 GTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCCACTGGAACA  
 ATAATGGAATTTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT  
 TGGGCATACAACTTTCAGGCCAAGCGAACCCAGAAACATTAATATTACAGTAACCTTCTCAGCAGCAAAATCTTCT  
 GTGCCCTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTCCTCCAGCCCAATGATTGTTTACGCAGAA  
 ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
 TTGGAATTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
 ACAGAAAATGGCAGATATAGCTTAAAAGTTCCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCTCCA  
 CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAAACCCGCCAAGCTGAAATGAT  
 GAGGATCTCAGACCACCTTGGAGGATTTTCAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAGTCCCAAGC  
 CTTCCCTTGCCCTGACCAATACCCACCAAGTCAAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATCTT  
 ACATGGACAGCACCAGGAGATAATTTGATGTTGGAAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACAAAGGAGGCCAACTCCAAGGAA  
 AGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCACATATTATTGCCATTTAAAGTATAGATAAA  
 AGCAATTTGACATCAAAAGTATCCAACATGCAAGTAACCTTTGTTTATCCCTCAAGCAAACTCTGATGACATTGAT  
 CCTACACCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTATTG  
 TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAAACGAAGAAAAAATCTT  
 AAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACAATGTAAGTAAAGGATATTCTGAATCTTAAATTCATCCCAT  
 GTGTGATCATAAACTCATAAAAAATAATTTAAGATGTCGGAAGGAGTACTTTGATTAAATAAAACACTCATGGATA  
 TGTAAGAACTGTCAAGATTAAATTTAATAGTTTCATTTATTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG  
 ATCCTTTTTCATCTGATACCTGGTTGTATATTATTGATGCAACAGTTTTCTGAAATGATATTTCAAATTCATCAA  
 GAAATTTAAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAAATAAACCAACATTTGGAAAAAATAA  
 AA



## FIGURE 71

CTCCTTAGGTGGAAACCTTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCGGGCAGGGGTGA  
CAACAGGTGTCTATCTTTTGTATCTCGTGTGTGGCTGCCTTCTTATTTCAGGAAAGACGCCAAGGTAATTTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTCTCTTAGCA  
GTGCTCAGAACTGACTTGCCTGAGGGTGGACCAGAAAGAAAGGTTCCCTCTTGTGTTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAA  
AGTAGAGAAGCTGCTGTGTGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGTTTCGCCGGGGGGCTGCTTGCCTGGATTTCGGGGTGGT  
GTTTTGCTGGTCTCTCTGTGTGTCTCTGTCTGTACATGTTGGCTGCACCCAAAAGGTGACGAGGAGCAG  
CTGGCACTGCCAGGGCCCAACAGCCCGGGGAAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACCTGAGCAGCCTGAAGCGGCAGATGCGACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAAGCAGCTCAGG  
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC  
CTGGCCCTTCTGCACTCGCAGGTGGACAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG  
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG  
AGGAAGGACAAGCGGGATGATTTGGTGGAGGCATTGAATCAGCCTTGGAGACCTTGAACAATCCTGCAGAGAACAGC  
CCCAATCACCGTCTTACACGGCCTCTGATTTTATAGAAAGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTAT  
GAGCTCACCTTCAAAGGGGACCAACACGAATCAAACGGCTCATCTTATTTTCGACCATTAGCCCCATCATGAAA  
GTGAAAATGAAAGCTCAACATGGCCACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAGTTTC  
CGGCAGTTTCAGAGAATTTAGGGAGATGTGCATTGAGCAGSATGGAGAGTCCATCTCACTGTTGTTTACTTTGGG  
AAAGAAGAAATAATGAAGTCAAAGGAATACTTGAACACACTTCCAAAGCTGCCAAGCTTCCAGAACTTTACCTTCATC  
CAGCTGAATGGAGAATTTCTCGGGAAAGGGACTTGATGTTGGAGCCGCTTCTGGAAGGGAAAGCAACGTCTTCTC  
TTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGA  
GTATTTTATCCAGTTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTTGAA  
CAGCAGCTGGTCATAAAGAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGAGAC  
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCGGAGCAGTACAAGATGTGCATGCACTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG  
GTGTTGAGGCAGGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAACATGAAGTCCCAAGA  
GAAGGATTGTGGGAGACACTTTTCTTCTCTTTCGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGCAAAAAGAAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAACAGA  
AATCAAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG  
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA  
AATATTGATGATTAAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAATATCAGAAGGCAGGAGAGATAGGCTTATTATGATACT  
AGTGAGTACATTAAGTAAATAAAATGGACCAGAAAAGAAAGAAACCATAAATATCGTGTCAATTTTCCCAAGAT  
TAACCAAAAAATATCTGCTTATCTTTTGGTGTCTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT  
TTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC  
ATTTTATATTTTAAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACT  
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAGAAATGAC  
ACTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTT  
CTCCTCAGAAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACATCTCTTTT  
AAAACAGGGTCTCCTCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATG  
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAG  
TAACTGAATTATTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAATTTGATTTTATTACCATTT  
CAAACATATTTTAAAAATAAATACAGTTAATAGAGTGGTTTCTTCAATCATGTGAAAATATTAGCCAGCACCAG  
ATGCATGAGCTAATTTATCTCTTTGAGTCTTCTGTTTGTCTCAGCTAAACTCATTTGTTTAAAGGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

## **FIGURE 72**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW  
EQHRNYVSSSLKRQIAQLKEELOERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN  
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLSQY  
NPGIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINICGFDLDIKGWGGEDVHLYR  
KYLHNLIVVRTPVRGLFHLWHEKRCMDLTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQXQKTSSKKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 315-319, 324-328

#### **N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

#### **Amidation site.**

amino acids 377-381



[illegible][illegible]

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPLPALQ  
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGGLPRKYVAAQLHLHWGQKSGPGGSEHQINSEAT  
FAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGTGTC  
TCTGGTGGTTTGCCTAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGCTCCTGACAGCTCC  
AGAGAAGTGGAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
AGGGCCCCCTCGCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTCTTTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTTATGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAG  
AAAACCGGAAGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTGAGAACCCTGACATTTGTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTTGAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA  
TCCCCAAACTGGCAGGCTGTGTATTTCCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCG  
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA  
TGTGCAGATGGAAACTGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAACAAGTGAG  
TCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT  
CTGTGAGAATTACTTATTTCTTTTCTATTTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSSSQIGPPEVALTTDEKSISSVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDKRFFVPAEK  
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLESQA  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 140-163

#### **N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
CTGGGAAGATGCGCGGCCCGTGGACCTTACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA  
TAAGCTCTCCTTCCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAAACAGCTGTGTCCCGTGATCGAGGCTTCCCTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA  
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCCCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGT  
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
CCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDHNATSILQQLPILLSAMREK  
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAKLDSQGKVT  
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT  
KGDQLIILNLNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTkdALVLTpasLWKpSSPVsq

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGAGGCCTCCTGGGATTC  
ATTCTGTGTGCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCAGTGGTGCCTGACAG  
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG  
CTGGAATCATCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACGATGCCTAC  
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAACAGCATGCAGGTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC  
TCACCTTGCTGCTCCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA  
GGACTCAGAGGATCCCTTTGCCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA  
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCA  
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

## **FIGURE 8o**

MASLGQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNHLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59



## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC  
CCCGCGTTCTCTTTCCACCTTCTCTTCTTCCCACCTTAGACCTCCCTTCTGCCCCTCCTTTCCCT  
GCCCACCGCTGCTTCTGCGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
GTTGATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTTCGTCTCCCTTCTCCCGACTCCGCTCCCGG  
ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT  
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCCT  
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGGCCCCACAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTTCCCGCCTGCCCAACCAGTGTGTCTCTCGAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCGAACCAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA  
GTGTGCAGTGCCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG  
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA  
TAAGAAGTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLFNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTY  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKAVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA  
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAG  
GACGCAGCATTCTCCTGTTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
ACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCACTCCTCGGGCTGGTTCCTCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTGTCC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGCTACAGATAG  
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
TTTTTTGGCATTGTGGACTGAAGATTTCTTCTCCAAATTCAGTGGAATAATCCAGGCGGAACCTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT  
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA  
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGCGTTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG  
TGAGTCCCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT  
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
CTGACATTACATTTAGTTTGTCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG  
AACCCTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT  
LNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPESTSSESSQATTPLPRGEM

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domain:**

amino acids 239-255

[illegible][illegible]

## **FIGURE 86**

MLLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPACEQGTPPMISWIGTSVSPDPSTTRS  
SVLTLPQPQDHGTSLTQVTFPGASVTTNKTVHLNVSYPQNLMTVTFQGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE  
DANAVRGASQGPLTEPWAEDSPDPQPPASARSSVGEGLQYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

### **Signal peptide:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCAATTTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGTGGCGGCTGGACCCTGGTGGCCAGCGTGTCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT  
GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVIIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298



## FIGURE 89

CTAGATTTGTGCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG  
CTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT  
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTCCAGCTG  
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTAATTACCTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA  
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCTCCCGGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGGCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCCGGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC  
CATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
TGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTC  
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGCTGTGTGTCCTCTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGGCCGAGAGCATGTGCTGGATCTGTTT  
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 93

CGGTGGCCATGACTGCGGCCGIGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTT  
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTGGGCTTTGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCAT  
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGTGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQXYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKCLLCQDKNFLLYNQRRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACCTTGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG  
GAACCCAGCAGGCCGCCCTCCCAACTCCCACTGGCAGATGACGACTTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATCTTAATT  
TACCTGAAAATATTCTTGAAATTTTCAAGAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAACATATTTGGAAAACCTGGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

Signal peptide:

amino acids 1-16



## FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTGACCATG  
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC  
 AGAGCTGTCTGTGGAAGTTCCAGAAACTATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC  
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG  
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGTGCTGACAGGGCCCTGGACCCGAGAGGA  
 GCAGGCAGAGTACCAGCTACAGGTCAACCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC  
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC  
 AGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCCTTCTCTTCTTCTGAGGCTTCAGACCG  
 GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC  
 CTTCCCCAGACATGTTCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
 CCAGGCCTCAGGCCACAGGCCACTGCCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGT  
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCACCACATGGCCAGGTA  
 CACTGGAGTGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAA  
 TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
 AGGTGCGGGCTCAGAAATCCCATGCGGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG  
 ATGGATGAGAATGACAACGTGCCATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA  
 ATTTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
 CAGGTGGACCCCACTTCAGGCAGTGTGACGTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
 CCTGCTTCTGGTGTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG  
 TCGAAGTCGAGTCACAGATATCAATGATCACGCCCCGTAGTTCATCACTTCCAGATTGGGCCCT  
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA  
 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGGCATTGAGAGGGGAGACACAGAAGGGACTTTTG  
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC  
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCCAAGTTGG  
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTCTCTGCTGACCATC  
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
 CTGCATTGAGAAATTTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA  
 TACCTCTGCACACCCCGCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT  
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCACGGGATTGGC  
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGT  
 GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT  
 CGTGTGTCTGCAACGTGGAGGGGAGTGCATGCCGAAGGTGGGCCGATGAAGGGCATGCCCA  
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTC  
 ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT  
 GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG  
 TCCCTGGGAGAGAGCCAGCAGCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA  
 TCTGCCCTGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT  
 TATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTGTTGCCCAATAATAAGCCCCAGAGAA  
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPFHSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFVEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPLRAGQNI LLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT  
IQSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQS LQGAQPGDTYTVLVEAQDTALT LAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGYPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWVEP  
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGCTTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC  
TCTGCCAACCTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACACCTCC  
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACTTCCCATAGTGATCTACTGCAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
CATGGCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG  
GTGGAGTCTAAGTGGTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGGCGCATTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCCAAGACCTGGTTTCTTTTCTTTCATTCATCCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAA  
AATCTTGAAGAAGGTATTCTTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACAGCAAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCTGCTTGTCACAGGTG  
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCAATTCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTCATGGAAAGGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATT  
TCATGCTGAGTCCCTTTTTTACCTTTGATGTTGTAAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT  
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGCATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGGAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAGAGGCTGCGTTCCTTCTATCAAG  
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC  
CTTGTTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTACGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG  
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGAATATTTCTTACT  
GCCATCATTATTTGTTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTT  
TTTAATCTCTGAATGTAATTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCIMRYSYLRLKICLKASLKGVPFGFGWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSKSRSNFAEKNGLOKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHLQGDFFPREIHFHVHRYPIDTLPTSKEQLWCHKRWEEKEERLSFYQGEKNF  
YFTGQSVIPPCKSELRLVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIEELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCACTGTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCCTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA  
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTCAGCCCTCACCTTGGCGCCTGGCTTCTA  
TTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGTTCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG  
TTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACA  
ATGTGACTTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTT  
ACATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT  
GGACTATGAGGGTGGGACCATCTCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTCTAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCTGCTTAAAGGGC  
CCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC  
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTGTAGTCACGG  
ACAGTGATTCCTGCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGACAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCACCATAAACTCTGTT  
TGCTTATTCACATTAATTTACTTTTCTCTATACCAATCACCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCAGCAT  
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCC  
CTCATTAAACACAGACACAAAAATCTAAATAAAATTTTAAACAAATAAACTAAACAATATATTTA  
AAGATGATATATACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAAATTTAAAT  
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEK  
TPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259



## FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTGGGAACCTGGGTTATCGGCCTCGTCACTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC  
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA  
ACACGAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
TTGTGAGTGTCTCACTGTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
ATAAAACCTTCGAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCCATCACA  
TGACTATGATATTTCTCTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTG  
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT  
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACC  
TCAAGCTTACAATGAGCCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
GCCAGGGTGACTCTGGAGGACCACCTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTG  
GATTACTTCAAAAACCTGGTATCTTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG  
GGTGTGGAGGCCATTTTATAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA  
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAAATTTGACTTGTGACATAAATTTGTAAT  
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCATTT  
TCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA  
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTATGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT  
ATAATAATTATACAACTTCATGCAATGTACTTGTCTTAAGCAAATTAAGCAAATATTTATTTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVI F ISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPSHDYDISLAELSSVPYPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTG  
CCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCCAGC  
GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
ACGGGGCTCACAATGGCCAGAGAAGATTCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA  
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTTAATGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTTCCT  
GTGGTTTCATCCGGTCATGATTGCTGTTTGTGTTTCTTATCATTGTGGGGATGTTAGGATATTG  
TGGAAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGTGTCATTTTCT  
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA  
GATATGGTCACCTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTGTAGAGAATCCCAGGATGTTCCAAA  
CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT  
TTTGAGAGGAACCAACAACACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
ACAGACCAATGATGTCCTTGAAGAATGACAACCTCTCAGCACCTGTCAATGTCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
TTGAGATGGAGGAGTTATAAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT  
TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAA  
TAACACCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA  
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAA  
CTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
CTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTCAATATTGGTGACT  
ACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
ATTTTTAGCCTTTCTGTAAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC  
TGTTATTTAAATACTTAACCCTAATTTTGAATAATACCAGTGTGATACATAGGAATCATTATTC  
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA  
AAGGACTTGTATGCTGTTTTTCTCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA  
GCTTATCTTTTGCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA  
TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAACATGTGACAATTTAGAGATT  
CTTTGTTTTATTCTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAA  
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTGTGTATTTGTTTTAT  
TTCTCAGAATATGGAAGAAAATTAATATGTGTCAATAAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT  
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTTCCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAG  
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGSCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCAGGCTGTGCCAGCT  
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACAGCGAGTGCACATCCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCCTGT  
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTTGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTTCTCTCAAGACATGTGGTACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
ACCTGCGAGTTTCCACGCCGTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT  
CATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTTCAAGTTTGTGGGCAAGACCACAAGGAAGTGTTCCTGCACTGCCGGTCTTGTCTGTGGAGTG  
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCAATGCGTCGTGGGCGAGGAGAGGACTCAGC  
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTCTAAGAACATCTGCCAACAGC  
TGGGTTCCAGACTTCACACTGTGAGTTCAGACTCCAGCACCAACTCACTCTGATTCTGGTCCATTAGTGGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGTTTCATCTTCTAGGGTTGAAAATAAACTGTCCA  
CCCAGAAAAGACACTCACCCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAGTTACTGAAATTATGA  
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGGAATTTGGAAGTGTATCAATAAAACAGTATATAATTTT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLDESQGPFLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNLSHPLEGDGIVQRQACASFNGNCCWNTTVEVKACPGGYVYRLTKPSVCFHV  
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFFRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHV  
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCCHRRMRGAGGEDSAGLQGQTLTGGPIDWED

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### **Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

#### **N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

#### **ZP domain proteins.**

amino acids 431-457

#### **Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGCTGACCAGGGAATTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCCGAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAACCTGGTTCTCTGCCTGTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCCTG  
TGGGAAGAGCCTGAAGACCCCCGTGTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA  
GCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG  
CTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
CTCGGGGGGGCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTGCAGTGTCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT  
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTTGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC  
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIEFNPMYPKDNIDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLOASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQCQDSGGPLMYQS  
DQWHVVGIVSWGYGCGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)



## FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTTTTTTGTTCTCTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTTCACCTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCTCGAAG  
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCAAGATTTATAGGCGATGGCTCCCACTGCCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCCCCATCTAACCTTTTCATGTCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCACTTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTTGCCAAATTATGGGTGAGAAAAGATG  
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA  
AACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAAT  
TTTGGGAGCCGAGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA  
TGTTTATTTGTAA

**FIGURE 114**

MLWWLVLLLLPTLKSVCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFGGFCPGRRRD

Signal peptide:

amino acids 1-15

## FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACTTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAACTTCCAATAAATGACTATACTGAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAAGTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-40

#### **Transmembrane domain:**

amino acids 25-47 (type II)

#### **N-glycosylation sites.**

amino acids 94-97, 180-183

#### **Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

#### **N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 315-317

#### **Cytochrome c family heme-binding site signature.**

amino acids 9-14

## FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
GGGCGGGCGGCCAGGATCATGTCACCACCACATGCCAAGTGGTGGCGTTCTCCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC  
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCTT  
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
TCTGTGTTTGCACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACGGCATGGGTGG  
GATGTGCAGACTGTTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA  
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTGCTTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCACGACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA  
CCCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTTCCACCATAAAACA  
GCTGAGTTATTTTATGAATTAGAGGCTATAGCTCAGATTTTCAATCCTCTATTTCTTTTTTAAATATAACT  
TTCTACTCTGATGAGAGATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
TTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT  
ACACTGTGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG  
TTGACATCTTCTTATTACAGCAACACCATTTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTCTGT  
CGCGGCTCAGAAATGTCCCTAGATGAATGAGAAAATATTTTTTTTAAATTAAGTCTTAATATAGTTAA  
AATAAATAATGTTTAGTAAATGATACACTATCTGTGAAATAGCCTCACCCTACATGTGGATAGAAG  
GAAATGAAAAATAATGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC  
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAAT  
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAAACTAATCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSVYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGCARTEDEVQSYPSKHDY  
V

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTTTAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGACCTACAGGCAGCCAGAG  
GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTGCCAAAAACGTGAGCTTGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTCTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAACTGCCT  
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGCAGAATGAGATA  
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
CTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGAACATTTATATCTCACATAGAGACATGCTTATATGGT  
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
TTTATAATGAAGATTAATAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
GCTGTTTTTTAGCCTAGCAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
CTTGTGTATTAAATTAACATTTTTAAAAACGCAGATATTTGTCAAGGGGCTTGCATTCAAACGCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
AAAATATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA  
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATGTGATTTTTGTTCTGTGAAAAATAAATTCCTTCTTGTA  
CCATTTCTGTTTAGTTTTACTAAAACTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAA  
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTTATATTAATAAATGTACATTTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

10063553



## FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG  
CCAGACGCTGACCACGTTCTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGCAGCC  
GGGAGCCATGCACCCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCCGCGCGTTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGCGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCCTGGACCCCACTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATCAACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTCACCTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG  
CTTCAATCAAAGTGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTGTTTTCTCTTAGTATAGCATTTTTA  
AAAAAATATAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
CTGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCTTGGGAAGAACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTA  
ACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG  
TGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGGTCCAATTTT  
TCTTCTGGGTGTCAGCGAGCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCATGCAACTG  
GCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGCAAAATGGTATATTGTGA  
ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
ATAACAGCCTTCAAAAACTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCAATACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA  
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT  
TACGGAACCTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
CGGAAGCTGCTGAGTTTACATTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC  
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGAATAAAATCAGTGT  
CATAGGACAGACCATGTCTTGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA  
TCGAAGCTTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT  
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTT  
TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT  
TGCCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT  
CTACGTGTCTGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA  
GATTATAAACCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGCAACCATTGTGATAAAAAGAGCTCTTAAAAAGCT  
GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC  
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCCGTTTTAGTGCATTATAATACT  
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
GAACCTCCGGTTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTT  
GTTTTAAGATAAAACTTCTTTTCATAGGTAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLLSLHLRSNSLRITPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLHLEHNQFSKLNALFPLVSLQNLQWNKISVIGQTMSTWSSLRDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKEQGVNVIDAVKNYSICGKSTTERFDLALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCITYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCGGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCGCGAGCT  
AGCAACCTTTCCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATTGCGATTTTCGTGGTGATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAAATCATGAC  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTCAAGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC  
ATCTTGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFFLDLTKTRLQMQGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP  
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCCAAGCAGGTGGCGGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGACGGCTACCCCGGGACTTTGATCCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCCTGCTCTCAGGCAGCACCAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA  
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT  
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG  
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGAAGTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCCTTCATGGCTTGCCTCCTGCTTGGATTTTAGGTGTTGATTTCTGGAT  
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGGATTTTATA  
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAGGAGGTGGTGTCCC  
TAATTGTTTTACTTGTAACTTGTCTTGTGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG  
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC  
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCCAGTGGATTTTCATGGTGATCATTAAGAAAGAAAATCGCAACCAA  
AAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPVSVTHFYSAKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

#### **Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114



## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAI  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC  
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGCTCGCGCTGTTTCATTTAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA  
TTAATTTTTTAAC TGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTAAC TGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACA  
GGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAACCTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAATGACAGGATTCGTTCTTAATTTCAATTAAAATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTTCAGAT  
TTGAAAACTTGCTGAAAGTAGAAGAATATACCTTATACCACAACAGTTTAGATGAATTCCTACCAACCT  
CCCAAAGTATGTAAGAGATTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCTGGGGTTT  
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTCAAG  
GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCTGGTGGGAATTCCTGACTGCTGCACCAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGGCCCCAAATGCTTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
GATGATTTGGACAATATAACACAACCTGATCTCTCGCAACAATCCCTGGTATGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTCCGTGGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTCTGTTGGATGGCTATTAAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATGTAAGC  
ACCATTCAGATAACCACTGCAATACCCAAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCAATCTCTTGGAACTTGCTCTACCTATG  
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAGTGAAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC  
CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG  
TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT  
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCTCTCTAATGGAATGAATCTGT  
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC  
TCACACTCATGATGTGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNDSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLNDITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRKTTITIVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCJETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44

## FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCAGGCTTCTTGGA  
GCCCTGCCGGGCCACTTGTCTTCAATGCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAAGCAGAG  
GCCGGCCATGGCCAGCCTGGGGCTGTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCCAGGAGCCCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCCTCCAGCCCGG  
GTTTTGGAAGCTCCACATGCTGATCCCACTGATGCCTCCTTGGTGTACCCACGTTCCGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCCTACCTACCCGGGACATCTTCATGGAACATCATGTTCTG  
TGGAAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTTTCAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC  
AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT  
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCTATACATCCTGGCAGAAATACCCCCAGCAACAGAGAGCCACCCATCCACACCG  
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSLSGLARAQGAERTVSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSYLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPDQSFSEE  
RSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQEGCGFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 39-56

#### **Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

#### **N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

#### **Amidation site.**

amino acids 10-14

#### **Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCGCTCTGTGGGGCTTCTTTCCCGTCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCA GTTGTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCCGAGTGTGGTAGACGGAGAAGAGCACGTGGTTCCTTAAG  
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAAAGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGTCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACCTGTGTATGTT  
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCCCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
RVLVDGEEHVGFLLKTDGSFVVDIPSGSYVVEVVS PAYREDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLP LLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

### **Important features of the protein:**

#### **Signal sequence:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 161-182

#### **N-glycosylation site.**

amino acids 184-187

#### **Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

#### **N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

#### **Amidation site.**

amino acids 238-241

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236



## FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAAACAA  
GTTTTGACATTTCCCCTGAAATGTCTTCTATCTATTCACTGCAAGTGCCTGCTGTTCAGGC  
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT  
TTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC  
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCTCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTTAA  
AACTACCAGACCCCTGACCATTATCTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGGAAC TAGACATTTCTGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA  
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT  
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA  
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATTTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATTCAGAAAGAGTGG  
CTAGGGGGGTATTCAATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTGATGTGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAAA  
AAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL RPEIF  
SSREAWQFFLLWSPDFRPMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGCATCCAGCC  
TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCCTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA  
CACGGAGCGGAGCCCCAGCGCCCAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG  
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
CCTTCTGGCTTTGTGACGCTCATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAGAAAGTATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA  
TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTGAGATTACACAGAGGT  
GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCC  
TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGCCCCAACAGCCCCCTGATTGGGCAG  
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAGGAGAGAGA  
GACGCGCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
GGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAA  
CCCGGTGATATCCGACATCCAAAGCACGTCCAAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
ACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCCGATTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG  
AATGTGCCGTGATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGG  
GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG  
TTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCAGTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
CTGTCATCTCCTGGGTTTTCTCTGCTCTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACGT  
CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT  
GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGTCAGTGCCTGGAC  
AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG  
TTACATCTGTGCTGTGAGTGCAGATGCCTCAGTTCTTGGAAAGCTAGGTTCTGCGACTGTTAC  
CAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAGAGACAATCGGCCTGGA  
CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCAAGATGCATCCT  
GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCCTAGTCCTTGGCC  
TCGGACACCTTCATTCGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC  
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
ACCCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTGTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG  
CCACGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAGATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPKHFVEYDGTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLEMSD S VLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC  
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCTGGGGTCTCTAAAGGGAGTTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCT  
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

cAMP- and cGMP-dependent protein kinase phosphorylation site.  
amino acids 33-36

amino acids 50-55, 87-92

amino acids 37-182

## FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCCTTCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTAGAGTGAACCCACTCACAGGCTTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTATCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAACATCAGCATTTTAAGAAAAAAAAAAAA  
AA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLGEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15



## FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACCTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

[illegible][illegible]

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

## FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCCCACCCACCCCTCCTGGCTCTTCCTGTTTTTACTCCTCCTTTTCATTGATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCGAGCGTGAAGAAATGGGGTT  
CCTCGGGACCGGCACTTGATTCTGGTGTAGTGTCCCGATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
TGTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTATGAAG  
AAAATGACAGAGCCGTTTGGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCCAATAAGCCCAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA  
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAAGAAGCAAAGAGAGAAAGAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT  
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTTGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGAAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA  
CTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAAATTTTTGACCCAAGG  
GTTATTAGAAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAAACATAGCTTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIAKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA  
GATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGGAAAG  
CCAGTGCCCTGTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGGCTCACC  
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAGACTCAGCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT  
GAGTGGAGGAGACCCATGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT  
CCACGGTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA  
CTGGGAATAACATGAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCT  
TAATGGTAAGTACAAGTGTACCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA  
GGGTCACTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCCAGCCCCACCCCTTCCCTTAAATCCTGCCACTGTCTATA  
TGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGATGTCTAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA  
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGTCTATGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTAATTAAAGATACCTATTATATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT  
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTCTACATGAAGATGA  
ATTCCCTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
TTGTCCTCAGCCTCCACTTCCCCAGAGTAAATCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
GTGGCTGGAATCTCTGGGTAAAGGAACCTTAAAGAACA AAAATCATCTGGTAATTTCTTCTAGAAG  
GATCACAGCCCCCTGGGATTTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG  
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTCATAT  
GACTGGTTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACCGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGGAAGAGGCAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAGAGAAAGATAAATTTTCGGCTGTTTTAA  
GCCACCAAGGATAAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT  
CTCCTCGTGTTTACATTCTGTGTGTGTCCCTCCCACAATGTACCAAAGTTGTCTTTGTGACCAA  
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCATATAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT  
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
AAGTTGCTCAGTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401</
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N-myristoylation sites.

Interleukin-1 signature.

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103



### FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGCGCCGC  
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
CCCTCTTGGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTC  
CAGCCTTATATGCAGGAGGTGGTGCCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTC  
TATACACAGAAAAACAATTTATTTTTTAATAATTGTCCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTCCATAATCAGTACTTTATATTTATAAA  
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFILMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCACTGCAGAGGGC  
TGCCAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT  
TGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGCGGCCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCCTGTGAAGTGTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACCTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAAA  
GTTCTGCCCATTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG  
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTATTGAATGTATAGAGATTTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLEDSSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTTTCATTGGGGCCCATATATTCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGAAGAAGAATGAGGAGACA  
GTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGAAGTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAAGGTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTCAAACCATTCGAGAAGTGAGGTTCCTTGAAA  
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVSWV  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGFPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
GCCSL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **Transmembrane domain:**

amino acids 290-309

#### **N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

#### **Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

#### **N-myristoylation site.**

amino acids 116-122

#### **Amidation site.**

amino acids 488-452

## FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCATGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCATCCAGCAA  
GAGACCCTGGTCCGCGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 16o**

MTVKTLHGPA<sup>1</sup>MVKY<sup>2</sup>LLLL<sup>3</sup>SILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSM<sup>4</sup>SRNIESRSTSPWNYTVTWDPNRY<sup>5</sup>PSEVVQAQCRNLGCINAQ<sup>6</sup>GKEDISMNSVPIQQETLVV  
RRKHQ<sup>7</sup>GCSVSFQLEKVLVTVGCTCVTPV<sup>8</sup>IHHVQ

### **Signal sequence:**

amino acids 1-30

### **N-glycosylation site.**

amino acids 83-87

### **N-myristoylation sites.**

amino acids 106-111, 136-141



## FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCTCTGGAGGCTGAAGAGGGATTTC  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCTT  
TGGCACTGGGCCGAAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCTGCGGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT  
CGTGCTGCTCCGGGCCCCGTGCTGGCGCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGAGCCTAGGAA  
TGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCTACTGCCCGCTGCGTCTCTGC  
TGGAGGTGCAAGTGCCTGTGCCCCCTTGTGCGATTTGGTCAGTCTGTGGGCTCTGTGGTATATGAC  
TGCTTCGAGGTGCCCTAGGGAGTGAAGTACGAATCTGGTCTTACTCAGCCCAGGTACGAGAA  
GGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACA  
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA  
CCACACAGACCTGGTTCCCTGCCTCTGTATTCAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCTGCAGAGCTGGCTGCTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT  
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCTGGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTACGGTG  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCTCTCAAAGA  
CGATGTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCA  
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG  
CTGCGCTTTCCCTCATCTCTCTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAA  
CAGGACGTCCGCTCGGGGGCGGCCAGGGGCCGCGCGGCTCTGCTCTCTACTCAGCCGATGA  
CTCGGGTTTCGAGCGCTGGTGGGGCGCCCTGGCGTCCGCCCTGTGCCAGCTGCCGCTGCGCGTGG  
CCGTAGACCTGTGGAGCCGTCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTCACGCGCAG  
CGGCGCCAGACCTGCAGGAGGGCGGCGTGGTGTCTGCTCTTCTCTCCCGGTGCGGTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCC  
GCGCCTCGCTCAGCTGCGTGTGCCCAGCTTCTTGCAGGGCCGGGCGCCCGGAGCTACGTGGGG  
GCCTGCTTCGACAGGCTGCTCCACCCGACGCCGTACCCGCCCTTTCCGACCGGTGCCCGTCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCGCGTTCG  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTC  
CATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAAGGGCGGGACCTGGGGCGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTCTAAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGPVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV  
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVSA DGNVHLVLNV  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG  
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRROTLEGGVVVLLFSP  
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT  
LPSQLPDLFGALQQPRAPRSGR LQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain.**

amino acids 453-475

### **N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

### **Glycosaminoglycan attachment site.**

amino acids 583-586

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

### **N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT  
 GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA  
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCAGCCACAGACACGGTCTACAGCATCGAGTATA  
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCCTGC  
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGACGACACTAC  
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCTTA  
 CCCCCACGCCAATCCGTGACGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG  
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
 ATATGAGTTCTTCGGCTGACCCCTGACACAGAGTTCCCTTGGCACCATCATGATTGCGTTCCCA  
 CCTGGGCCAAGGAGAGTGGCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
 TACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCGTCGCAGTACTCTGCTACCTGAG  
 CTACAGATATGTCAACCAAGCCGCTGCCACTCCAACTCCCTGAACGTCCAGCGAGTCTGACTT  
 TCCAGCCGCTGCGCTTTCATCCAGGAGCAGCTCCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
 AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAACGCTGCCCTGAG  
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCGAAGCTCAATTCCCATTCTACGCCCCACA  
 GGCCATCTCTAAGGTCCAGCCTTCTCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
 CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAA  
 CACCTTAGGCCCTAAGGTGACGTTTCAAGAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATGCAACAGC  
 CCTTGGGGATTTCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA  
 CCACAGTACCTAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
 CCTCCCTTTGCAACCTCCTTCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
 GAGCAGCCACAGAAGTGGATTCTCTTTTCAGAGGCCCTGGCCCTGACTGTGAGTGGGAGTCTTG  
 AGGGGAATGGGAAAGGCTTGGTGCTTCCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA  
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA  
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGGTGCTCGCTGAGCCCTG  
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC  
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCCTCTCCTTGCCCCATTCTTGCCAGTTTC  
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTGATTGTTCAAAGGTGGGAAGAGA  
 GCCTGGAAAAGAACAGGCCTGAAAAGAACAGAGGAGGCTGGGCAGAACAGAACACCTGC  
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCTGCAGCTCA  
 TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTTCATTCCTCTGATAGAACAAAGC  
 GAAATGCAGGTCCACAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGTTTCAGACCCCT  
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
 TGTACTGATGTACAACCTTTGCAAGCTCTGCCTTGGGTTGAGCCATCTGGGCTCAAATTCAGC  
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCTC  
 ATCTGTAATGTGGGGATCATACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
 TCTTTAAAGTGCTTAATAGTGCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA  
 AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDVTYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCTIS  
KVRSIQIMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLDPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTTFQPLRFIQEHVLIPIVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPSPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSIAM  
EESQEAQSLHQPLGICTDRSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGSPWGLLESVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTIVQWES

### **Signal sequence.**

amino acids 1-17

### **Transmembrane domain.**

amino acids 233-250

### **N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

### **N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA  
AGTGTGTAACACAGTTTTGGATATTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTGAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTTTCGTTGGCATCAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCATTTTGTAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGDEECSMVMYRGKALEDFTGPD CRFVN  
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDVPVEPEAFRAEDSEGEA  
FSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCCTAACTTC  
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAACCTCAGCCCCGCACATCCACGCGCGGCACAGG  
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCCGGCAGCTGGGCTCGGGC  
GGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG  
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTTCAGC  
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAC  
GTCCAGCCGAGTGAGCTTTTCAGGAGGCACGCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA  
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG  
TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATTCCCAGTACCGAAACTGGTACACAG  
ATGAACCTTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGC  
CTTGGGGGTCCCTACCTTTACCAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG  
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT  
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAACACAGTCTACACTGTGGATTTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCT  
GGATCTGTATAAGGAATGGCATCAGAACATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC  
AAGATGAACTGTAAGCTCCCCCTTGAGGCAATATTAAAGTAATTTTATATGTCTATTATTTCA  
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA  
ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAAGCAATTCCTTTTATTTCTTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAA  
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTTTGATAAAA  
ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG  
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT  
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA  
AATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT  
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAAATTAACAGATT  
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG  
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCCGGGGTTTGGG  
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG  
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTTGG  
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT  
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTC  
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTCTTGGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFRRVSVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-  
145, 212-217